

SEQUENCE LISTING

<110> Istituto Di Ricerche Di Biologia Molecolare P. Angeletti S.P.A.

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND
USES THEREOF

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<150> 60/635,791

<151> 2004-12-14

<150> 60/543,649

<151> 2004-02-11

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<210> 1

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 1

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31

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<213> Artificial Sequence

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<223> PCR Primer

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 <223> CEA-LTA fusion

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 gcagcctcta acccacctgc acagtactct tggtttgtca atgggacttt ccagcaatcc 840
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<210> 8

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 8

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          20          25          30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
          35          40          45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
          50          55          60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65          70          75          80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
          85          90          95

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Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu		
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Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys		
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Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln		
			180					185					190				
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn		
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Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg		
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Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu		
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Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr		
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Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr		
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Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp		
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Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn		
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Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser		
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Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro		
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<210>	9
<211>	2355
<212>	DNA

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 9

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taccgggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccctg ggaggacaag 480
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<210> 10

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 10

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Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
          20          25          30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
          35          40          45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
          50          55          60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65          70          75          80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
          85          90          95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
          100          105          110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
          115          120          125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
          130          135          140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145          150          155          160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
          165          170          175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
          180          185          190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
          195          200          205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
210          215          220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225          230          235          240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
          245          250          255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
          260          265          270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
          275          280          285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
290          295          300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305          310          315          320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
          325          330          335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
          340          345          350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
          355          360          365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
          370          375          380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385          390          395          400
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          405          410          415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
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Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
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Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
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Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
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Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
    515                                520                                525
Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
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Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
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Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
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Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
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Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
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Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
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Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
    625                                630                                635                                640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
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Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
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Thr Val Ser Ala Ser Gly Thr Leu Asp Ala Pro Gln Ser Ile Thr Glu
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Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
    690                                695                                700
Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
    705                                710                                715                                720
Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
    725                                730                                735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
    740                                745                                750
Leu Arg Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val
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<210> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEAopt-LTB fusion

<400> 11


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gccaccggcc gcaacaacag catcgtgaag agcatcaccg tgagcgccag cggcacctct 2040
agagctcccc agactattac agaactatgt tcggaatatc gcaacacaca aatatatac 2100
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accaaaattg ataaattatg tgtatggaat aataaaaccc ccaattcaat tgcggcaatc 2340
agtatggaaa actag 2355

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<210> 12

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> CEAOpt-LTBopt fusion

<400> 12

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accccccttca acgtggccga gggcaaggag gtgctgctgc tgggtgcacaa cctgccccag 180
cacctgttcg gctacagctg gtacaagggc gagcgctggg acggcaaccg ccagatcatc 240
ggctacgtga tcggcaccca gcaggccacc cccggccccg cctacagcgg ccgcgagatc 300

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atctacccca acgccagcct gctgatccag aacatcatcc agaacgacac cggcttctac 360
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taccctcgagc tgcccaagcc cagcatcagc agcaacaaca gcaagcccgt ggaggacaag 480
gacgccgtgg ccttcacctg cgagcccagc acccaggacg ccacctacct gtgggtgggtg 540
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agcatggaga attgataa 2358

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<210> 13

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEAopt-LTBopt fusion

<400> 13

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Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
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Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
          20          25          30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
          35          40          45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
          50          55          60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65          70          75          80

```

Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser	85	90	95
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile	100	105	110
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp	115	120	125
Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu	130	135	140
Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys	145	150	155
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr	165	170	175
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln	180	185	190
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn	195	200	205
Asp	Thr	Ala	Ser	Tyr	Lys	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser	Ala	Arg	210	215	220
Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro	225	230	235
Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn	245	250	255
Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	Trp	Phe	260	265	270
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn	275	280	285
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser	290	295	300
Asp	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Thr	Ile	Thr	Val	Tyr	Ala	305	310	315
Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu	325	330	335
Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr	340	345	350
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	355	360	365
Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr	370	375	380
Arg	Asn	Asp	Val	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Glu	Leu	Ser	385	390	395
Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	405	410	415
Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn	420	425	430
Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser	435	440	445
Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile	450	455	460
Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn	465	470	475
Asn	Ser	Ala	Ser	Gly	His	Ser	Arg	Thr	Thr	Val	Lys	Thr	Ile	Thr	Val	485	490	495
Ser	Ala	Glu	Leu	Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	500	505	510

Val	Glu	Asp	Lys	Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Ala	Gln
		515					520					525			
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Gly	Gln	Ser	Leu	Pro	Val	Ser
		530				535					540				
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn
545					550					555					560
Val	Thr	Arg	Asn	Asp	Ala	Arg	Ala	Tyr	Val	Cys	Gly	Ile	Gln	Asn	Ser
			565						570					575	
Val	Ser	Ala	Asn	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asp	Val	Leu	Tyr	Gly
			580					585					590		
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Ser	Ser	Tyr	Leu	Ser	Gly
		595					600					605			
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Ala	Ser	Asn	Pro	Ser	Pro	Gln
		610				615					620				
Tyr	Ser	Trp	Arg	Ile	Asn	Gly	Ile	Pro	Gln	Gln	His	Thr	Gln	Val	Leu
625					630					635					640
Phe	Ile	Ala	Lys	Ile	Thr	Pro	Asn	Asn	Asn	Gly	Thr	Tyr	Ala	Cys	Phe
			645						650					655	
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Ser	Ile
		660						665					670		
Thr	Val	Ser	Ala	Ser	Gly	Thr	Ser	Arg	Ala	Pro	Gln	Ser	Ile	Thr	Glu
		675					680					685			
Leu	Cys	Ser	Glu	Tyr	Arg	Asn	Thr	Gln	Ile	Tyr	Thr	Ile	Asn	Asp	Lys
		690				695					700				
Ile	Leu	Ser	Tyr	Thr	Glu	Ser	Met	Ala	Gly	Lys	Arg	Glu	Met	Val	Ile
705					710					715					720
Ile	Thr	Phe	Lys	Ser	Gly	Ala	Thr	Phe	Gln	Val	Glu	Val	Pro	Gly	Ser
			725						730					735	
Gln	His	Ile	Asp	Ser	Gln	Lys	Lys	Ala	Ile	Glu	Arg	Met	Lys	Asp	Thr
		740						745					750		
Leu	Arg	Ile	Thr	Tyr	Leu	Thr	Glu	Thr	Lys	Ile	Asp	Lys	Leu	Cys	Val
		755					760					765			
Trp	Asn	Asn	Lys	Thr	Pro	Asn	Ser	Ile	Ala	Ala	Ile	Ser	Met	Glu	Asn
		770				775						780			

<210> 14

<211> 2358

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 14

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cgccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
agctgcgtga tccgcaccca gcagatcacc cccggccccc cccacagcgg ccgcgagacc 300
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accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgccaagcc ctacatcagc agcaacaaca gcaaccccgt ggaggacaag 480
gacgccgtgg ccctgacctg cgagcccagc acccaggaca ccacctacct gtggtgggtg 540

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aacaaccaga gcctgcccgt gagccccgc ctggagctga gcagcgacaa cgcaccctg 600
accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
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<210> 15

<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEAopt-LTBopt fusion

<400> 15

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Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
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Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
          20          25          30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
          35          40          45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
          50          55          60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
65          70          75          80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
          85          90          95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
          100          105          110

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Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115 120 125
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180 185 190
 Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195 200 205
 Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210 215 220
 Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
 245 250 255
 Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
 290 295 300
 Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
 325 330 335
 Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
 500 505 510
 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530 535 540

Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
 Ser Val Ser Ser Gly Asp Ser Ser Arg Ala Pro Gln Ser Ile Thr Glu
 675 680 685
 Leu Cys Ser Glu Tyr Arg Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys
 690 695 700
 Ile Leu Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile
 705 710 715 720
 Ile Thr Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser
 725 730 735
 Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
 740 745 750
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 755 760 765
 Trp Asn Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
 770 775 780

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 <211> 2118
 <212> DNA
 <213> Macaca mulatta

<400> 16
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 aggccgttca atgttgacaga ggggaaggag gttctttctac ttgcccacaa tgtgtcccag 180
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gtgaccttaa	cctgtgaacc	tgagactcag	gacacaacct	acctgtggtg	ggtaaacaat	1080
cagagcctct	cggtcagttc	caggctggag	ctgtccaatg	acaacaggac	cctcactgta	1140
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<210> 17

<211> 2118

<212> DNA

<213> Macaca mulatta

<400> 17

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<210> 18

<211> 705

<212> PRT

<213> Macaca mulatta

<400> 18

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      20           25           30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
      35           40           45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
      50           55           60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
      65           70           75           80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
      85           90           95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
      100          105          110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
      115          120          125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130          135          140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
      145          150          155          160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
      165          170          175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
      180          185          190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
      195          200          205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
      210          215          220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
      225          230          235          240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
      245          250          255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
      260          265          270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
      275          280          285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
      290          295          300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
      305          310          315          320

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Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
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 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
 355 360 365
 Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
 370 375 380
 Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
 385 390 395 400
 Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
 420 425 430
 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Ser
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
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 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
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 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
 Ser Val Ser Ser Gly Asp Ser Ala Pro Gly Ser Ser Gly Leu Ser Ala
 675 680 685
 Arg Ala Thr Val Gly Ile Ile Ile Gly Met Leu Val Gly Val Ala Leu
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 Met
 705

<210> 19
 <211> 705
 <212> PRT

<213> Macaca mulatta

<400> 19

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Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
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      20          25          30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
      35          40          45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
      50          55          60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
      65          70          75          80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
      85          90          95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
      100          105          110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
      115          120          125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
      130          135          140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
      145          150          155          160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
      165          170          175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
      180          185          190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
      195          200          205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
      210          215          220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
      225          230          235          240
Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn Leu Asn
      245          250          255
Leu Thr Cys His Ala Ala Ser Asn Pro Thr Ala Gln Tyr Phe Trp Phe
      260          265          270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
      275          280          285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His Asn Ser
      290          295          300
Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val Tyr Ala
      305          310          315          320
Glu Leu Pro Lys Pro Tyr Ile Thr Ser Asn Asn Ser Asn Pro Ile Glu
      325          330          335
Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr
      340          345          350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser Ser Arg
      355          360          365
Leu Glu Leu Ser Asn Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro
      370          375          380
Arg Asn Asp Thr Thr Phe Tyr Glu Cys Glu Thr Gln Asn Pro Val Ser
      385          390          395          400
Val Arg Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp
      405          410          415

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Ala Pro Thr Ile Ser Pro Leu Asn Thr Pro Tyr Arg Ala Gly Glu Asn
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 Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Ala Ala Gln Tyr Phe
 435 440 445
 Trp Phe Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile
 450 455 460
 Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Met Cys Gln Ala His
 465 470 475 480
 Asn Ser Ala Thr Gly Leu Asn Arg Thr Thr Val Thr Ala Ile Thr Val
 485 490 495
 Tyr Val Glu Leu Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro
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 Ile Glu Asp Lys Asp Ala Val Thr Leu Thr Cys Glu Pro Val Ala Glu
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 Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
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 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
 545 550 555 560
 Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
 565 570 575
 Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ser Lys Ile Thr Ser Asn Asn Asn Gly Ala Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
 660 665 670
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 Arg Ala Thr Val Gly Ile Ile Ile Gly Met Leu Val Gly Val Ala Leu
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 Met
 705

<210> 20
 <211> 702
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60

Tyr	Ser	Trp	Tyr	Lys	Gly	Glu	Arg	Val	Asp	Gly	Asn	Arg	Gln	Ile	Ile
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Gly	Tyr	Val	Ile	Gly	Thr	Gln	Gln	Ala	Thr	Pro	Gly	Pro	Ala	Tyr	Ser
				85					90					95	
Gly	Arg	Glu	Ile	Ile	Tyr	Pro	Asn	Ala	Ser	Leu	Leu	Ile	Gln	Asn	Ile
			100					105					110		
Ile	Gln	Asn	Asp	Thr	Gly	Phe	Tyr	Thr	Leu	His	Val	Ile	Lys	Ser	Asp
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Leu	Val	Asn	Glu	Glu	Ala	Thr	Gly	Gln	Phe	Arg	Val	Tyr	Pro	Glu	Leu
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Pro	Lys	Pro	Ser	Ile	Ser	Ser	Asn	Asn	Ser	Lys	Pro	Val	Glu	Asp	Lys
145					150					155					160
Asp	Ala	Val	Ala	Phe	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Ala	Thr	Tyr
				165					170					175	
Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg	Leu	Gln
			180					185					190		
Leu	Ser	Asn	Gly	Asn	Arg	Thr	Leu	Thr	Leu	Phe	Asn	Val	Thr	Arg	Asn
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Arg	Ser	Asp	Ser	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp	Ala	Pro
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Thr	Ile	Ser	Pro	Leu	Asn	Thr	Ser	Tyr	Arg	Ser	Gly	Glu	Asn	Leu	Asn
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Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn
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Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Thr	Cys	Gln	Ala	His	Asn	Ser
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Glu	Pro	Pro	Lys	Pro	Phe	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Val	Glu
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Asp	Glu	Asp	Ala	Val	Ala	Leu	Thr	Cys	Glu	Pro	Glu	Ile	Gln	Asn	Thr
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Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Pro	Val	Ser	Pro	Arg
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Leu	Gln	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Leu	Leu	Ser	Val	Thr
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Val	Asp	His	Ser	Asp	Pro	Val	Ile	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp
				405					410					415	
Asp	Pro	Thr	Ile	Ser	Pro	Ser	Tyr	Thr	Tyr	Tyr	Arg	Pro	Gly	Val	Asn
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Leu	Ser	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Pro	Ala	Gln	Tyr	Ser
		435					440					445			
Trp	Leu	Ile	Asp	Gly	Asn	Ile	Gln	Gln	His	Thr	Gln	Glu	Leu	Phe	Ile
	450					455					460				
Ser	Asn	Ile	Thr	Glu	Lys	Asn	Ser	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Asn
465					470					475					480
Asn	Ser	Ala	Ser	Gly	His	Ser	Arg	Thr	Thr	Val	Lys	Thr	Ile	Thr	Val
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Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
      530                      535                      540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
545      550                      555                      560
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
      565                      570                      575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
      580                      585                      590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
      595                      600                      605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
      610                      615                      620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
625      630                      635                      640
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
      645                      650                      655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
      660                      665                      670
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Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
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 <213> Artificial Sequence

<220>
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 <213> Artificial Sequence

<220>
 <223> CEA-FRC fusion

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<211> 2664

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-FcIgG fusion

<400> 25

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<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LAMP fusion

<400> 26

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<210> 27

<211> 3921

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-HSP70 fusion

<400> 27

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<210> 28

<211> 3585

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-VSVG fusion

<400> 28

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<211> 36

<212> DNA

<213> Artificial Sequence

<220>
<223> PCR primer

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<210> 30
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<220>
<223> PCR primer

<400> 30
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<210> 31
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<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 31
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<210> 33
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<220>
<223> PCR primer

<400> 33
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<210> 34
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<220>
<223> PCR primer

<400> 34
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<210> 35
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<220>
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<400> 35
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<210> 36
<211> 39
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<220>
<223> PCR primer

<400> 36
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<220>
<223> PCR primer

<400> 41
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<210> 42
<211> 36
<212> DNA
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<220>
<223> PCR primer

<400> 42
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<210> 43
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 43
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<210> 44
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer

<400> 44

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31

<210> 45

<211> 952

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-Dom fusion

<400> 45

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 20      25      30
Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35      40      45
Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50      55      60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65      70      75      80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85      90      95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100     105     110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115     120     125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130     135     140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145     150     155     160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165     170     175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180     185     190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195     200     205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210     215     220
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 225     230     235     240
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 245     250     255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
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Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
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 405 410 415
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 565 570 575
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 595 600 605
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 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
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 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
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 Thr Val Ser Ala Ser Gly Thr Ser Arg Ser Thr Pro Ile Pro Phe Ser
 675 680 685
 Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Asp Ile Asp
 690 695 700
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Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu
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 Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
 770 775 780
 Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr
 785 790 795 800
 Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly
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 Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp
 820 825 830
 Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys
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 850 855 860
 Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly
 865 870 875 880
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 930 935 940
 Gly Asn Pro Leu Arg Tyr Asp Thr
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 <211> 907
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-FcIgG fusion

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 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
 65 70 75 80
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
 85 90 95
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
 100 105 110
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
 115 120 125

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130 135 140
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
 145 150 155 160
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
 165 170 175
 Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
 180 185 190
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
 195 200 205
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
 210 215 220
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225 230 235 240
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
 245 250 255
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
 260 265 270
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
 275 280 285
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
 290 295 300
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
 305 310 315 320
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
 325 330 335
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
 340 345 350
 Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
 355 360 365
 Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
 370 375 380
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
 385 390 395 400
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
 405 410 415
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 420 425 430
 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 435 440 445
 Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 450 455 460
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 465 470 475 480
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 485 490 495
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 500 505 510
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 515 520 525
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 530 535 540
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 545 550 555 560

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 565 570 575
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 580 585 590
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 595 600 605
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 610 615 620
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 625 630 635 640
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 645 650 655
 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 660 665 670
 Thr Val Ser Ala Ser Gly Thr Ser Arg Lys Thr His Thr Cys Pro Pro
 675 680 685
 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
 690 695 700
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 705 710 715 720
 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
 725 730 735
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 740 745 750
 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 755 760 765
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 770 775 780
 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 785 790 795 800
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
 805 810 815
 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 820 825 830
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 835 840 845
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 850 855 860
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 865 870 875 880
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 885 890 895
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 900 905

<210> 47

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> DOM

<400> 47

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attatatcag atatatctgg gtttaattca tctgtaataa catatccaga tgctcaattg 180
gtgcccggaa taaatggcaa agcaatacat ttagtaaaca atgaatcttc tgaagttata 240
gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgttagcttt 300
tggttgaggg ttcctaaagt atctgctagt catttagaac aatatggcac aaatgagtat 360
tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctgggtg gagtgtatca 420
cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 480
acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggtttttata 540
actattacta atgatatgatt atcttctgct aatttgata taaatggagt acttatggga 600
agtgcagaaa ttactggttt aggagctatt agagaggata ataataaac attaaaacta 660
gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaa 720
gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 780
agagacttct ggggaaaccc tttacgatat gatacagata ggtag 825

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<210> 48

<211> 274

<212> PRT

<213> Artificial Sequence

<220>

<223> DOM

<400> 48

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Asp Ser Thr Pro Ile Pro Phe Ser Tyr Ser Lys Asn Leu Asp Cys Trp
1      5      10      15
Val Asp Asn Glu Asp Ile Asp Val Ile Leu Lys Lys Ser Thr Ile
20      25      30
Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile Ser Asp Ile Ser Gly Phe
35      40      45
Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala Gln Leu Val Pro Gly Ile
50      55      60
Asn Gly Lys Ala Ile His Leu Val Asn Asn Glu Ser Ser Glu Val Ile
65      70      75      80
Val His Lys Ala Met Asp Ile Glu Tyr Asn Asp Met Phe Asn Asn Phe
85      90      95
Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His Leu
100     105     110
Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile Ile Ser Ser Met Lys Lys
115     120     125
His Ser Leu Ser Ile Gly Ser Gly Trp Ser Val Ser Leu Lys Gly Asn
130     135     140
Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala Gly Glu Val Arg Gln Ile
145     150     155     160
Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn Ala Tyr Leu Ala Asn Lys
165     170     175
Trp Val Phe Ile Thr Ile Thr Asn Asp Arg Leu Ser Ser Ala Asn Leu
180     185     190
Tyr Ile Asn Gly Val Leu Met Gly Ser Ala Glu Ile Thr Gly Leu Gly
195     200     205
Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu Lys Leu Asp Arg Cys Asn
210     215     220
Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys Phe Arg Ile Phe Cys Lys
225     230     235     240

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```
<210> 49
<211> 2857
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA-DOM fusion
```

- 41 -

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gtgcataaag ctatggatat tgaatataat gatatgttta ataattttac cgttagcttt 2340
tgggttgaggg ttcctaaagt atctgctagt cathtagaac aatatggcac aatgagtat 2400
tcaataatta gctctatgaa aaaacatagt ctatcaatag gatctgggtg gagtgtatca 2460
cttaaaggta ataacttaat atggacttta aaagattccg cgggagaagt tagacaaata 2520
acttttaggg atttacctga taaatttaat gcttatttag caaataaatg ggtttttata 2580
actattacta atgatagatt atcttctgct aatttgata taaatggagt acttatggga 2640
agtgcagaaa ttactggttt aggagctatt agagaggata ataataaac attaaaacta 2700
gatagatgta ataataataa tcaatacgtt tctattgata aatttaggat attttgcaaa 2760
gcattaaatc caaaagagat tgaaaaatta tacacaagtt atttatctat aaccttttta 2820
agagacttct ggggaaaccc tttacgatat gatatag 2857

```

<210> 50

<211> 2859

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 50

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accgccagcc tgctgacctt ctggaacccc cccaccaccg cccagctgac catcgagagc 120
cgccccctca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcacccgc 240
agctgcgtga tccgcaccca gcagatcacc cccggccccg cccacagcgg ccgcagagacc 300
atcgacttca acgccagcct gctgatccac aacgtgacct agagcgacac cggcagctac 360
accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
taccgccagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccggt ggaggacaag 480
gacgccgtgg ccctgacctg cgagcccagc acccaggaca ccacctacct gtggtgggtg 540
aacaaccaga gcctgcccgt gagccccgcg ctggagctga gcagcgacaa ccgcaccctg 600
accgtgttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
gtgagcgtgc gccgcagcga ccccgtagac ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
gccgccagca accccaccgc ccagtacttc tggttcgtga acggcacctt ccagcagagc 840
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cccaagccct acatcagcag caacaacagc aaccccatcg aggacaagga cggcgtgacc 1560
ctgacctgcg agcccggtgg cgagaacacc acctacctgt ggtgggtgaa caaccagagc 1620
ctgagcgtga gccccgcct gcagctgagc aacggcaacc gcatcctgac cctgctgagc 1680
gtgaccgca acgacaccgg cccctacgag tgcggcatcc agaacagcga gagcgccaag 1740
cgagcgacc ccgtgaccct gaacgtgacc tacggccccg acaccccat catcagcccc 1800
ccgacctga gctaccgcag cggcgccaac ctgaacctga gctgccacag cgacagcaac 1860
cccagcccc agtacagctg gctgatcaac ggcaccctgc gccagcacac ccagtgctg 1920
ttcatcagca agatcaccag caacaacagc ggcgcctacg cctgcttcgt gagcaacctg 1980
gccaccggcc gcaacaacag catcgtgaag aacatcagcg tgagcagcgg cgacagctct 2040

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agaagcaccc ccattccatt cagctacagc aagaacctgg actgctgggt ggacaacgag 2100
gaggacatcg acgtgatcct gaagaagagc accatcctga acctggacat caacaacgac 2160
atcatcagcg acatcagcgg cttcaacagc agcgtgatca cctaccccga cgcccagctg 2220
gtgcccggca tcaacggcaa ggccatccac ctggtgaaca acgagagcag cgagggtgatc 2280
gtgcacaagg ccatggacat cgagtacaac gacatgttca acaacttcac cgtgagcttc 2340
tggctgagag tgcctaaggt gagcgccagc cacctggagc agtacggcac caacgagtac 2400
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accttcagag acctgcccga caagttcaat gcctacctgg ccaacaagtg ggtgttcac 2580
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agcgccgaga tcaccggcct gggcgccatc agagaggaca acaacatcac cctgaagctg 2700
gacagatgca acaacaacaa ccagtacgtg agcatcgaca agttccggat cttctgcaag 2760
gccctgaacc ccaaggagat cgagaagctg tacaccagct acctgagcat caccttcctg 2820
agagacttct ggggcaaccc cctgagatac gacacctag 2859

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<210> 51

<211> 952

<212> PRT

<213> Artificial Sequence

<220>

<223> rhCEA-DOMopt fusion

<400> 51

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Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
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Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
 20      25      30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
 35      40      45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
 50      55      60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
 65      70      75      80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
 85      90      95
Gly Arg Glu Thr Ile Asp Phe Asn Ala Ser Leu Leu Ile His Asn Val
 100     105     110
Thr Gln Ser Asp Thr Gly Ser Tyr Thr Ile Gln Val Ile Lys Glu Asp
 115     120     125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
 130     135     140
Pro Lys Pro Tyr Ile Ser Ser Asn Asn Ser Asn Pro Val Glu Asp Lys
 145     150     155     160
Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Thr Gln Asp Thr Thr Tyr
 165     170     175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Glu
 180     185     190
Leu Ser Ser Asp Asn Arg Thr Leu Thr Val Phe Asn Ile Pro Arg Asn
 195     200     205
Asp Thr Thr Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Val Arg
 210     215     220
Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
 225     230     235     240

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Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn	Leu	Asn		
				245					250					255			
Leu	Thr	Cys	His	Ala	Ala	Ser	Asn	Pro	Thr	Ala	Gln	Tyr	Phe	Trp	Phe		
			260					265					270				
Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile	Pro	Asn		
		275					280					285					
Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His	Asn	Ser		
	290					295					300						
Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val	Tyr	Ala		
305				310						315					320		
Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Thr	Ser	Asn	Asn	Ser	Asn	Pro	Ile	Glu		
				325				330						335			
Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Glu	Thr	Gln	Asp	Thr		
			340					345					350				
Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser	Ser	Arg		
		355					360					365					
Leu	Glu	Leu	Ser	Asn	Asp	Asn	Arg	Thr	Leu	Thr	Val	Phe	Asn	Ile	Pro		
	370					375					380						
Arg	Asn	Asp	Thr	Thr	Phe	Tyr	Glu	Cys	Glu	Thr	Gln	Asn	Pro	Val	Ser		
385					390				395						400		
Val	Arg	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Leu	Tyr	Gly	Pro	Asp		
				405					410					415			
Ala	Pro	Thr	Ile	Ser	Pro	Leu	Asn	Thr	Pro	Tyr	Arg	Ala	Gly	Glu	Asn		
			420					425					430				
Leu	Asn	Leu	Ser	Cys	His	Ala	Ala	Ser	Asn	Pro	Ala	Ala	Gln	Tyr	Ser		
		435					440				445						
Trp	Phe	Val	Asn	Gly	Thr	Phe	Gln	Gln	Ser	Thr	Gln	Glu	Leu	Phe	Ile		
	450					455					460						
Pro	Asn	Ile	Thr	Val	Asn	Asn	Ser	Gly	Ser	Tyr	Met	Cys	Gln	Ala	His		
465					470					475					480		
Asn	Ser	Ala	Thr	Gly	Leu	Asn	Arg	Thr	Thr	Val	Thr	Ala	Ile	Thr	Val		
				485					490					495			
Tyr	Val	Glu	Leu	Pro	Lys	Pro	Tyr	Ile	Ser	Ser	Asn	Asn	Ser	Asn	Pro		
		500						505					510				
Ile	Glu	Asp	Lys	Asp	Ala	Val	Thr	Leu	Thr	Cys	Glu	Pro	Val	Ala	Glu		
		515					520					525					
Asn	Thr	Thr	Tyr	Leu	Trp	Trp	Val	Asn	Asn	Gln	Ser	Leu	Ser	Val	Ser		
	530				535					540							
Pro	Arg	Leu	Gln	Leu	Ser	Asn	Gly	Asn	Arg	Ile	Leu	Thr	Leu	Leu	Ser		
545					550				555						560		
Val	Thr	Arg	Asn	Asp	Thr	Gly	Pro	Tyr	Glu	Cys	Gly	Ile	Gln	Asn	Ser		
				565					570					575			
Glu	Ser	Ala	Lys	Arg	Ser	Asp	Pro	Val	Thr	Leu	Asn	Val	Thr	Tyr	Gly		
			580					585					590				
Pro	Asp	Thr	Pro	Ile	Ile	Ser	Pro	Pro	Asp	Leu	Ser	Tyr	Arg	Ser	Gly		
		595					600					605					
Ala	Asn	Leu	Asn	Leu	Ser	Cys	His	Ser	Asp	Ser	Asn	Pro	Ser	Pro	Gln		
		610				615					620						
Tyr	Ser	Trp	Leu	Ile	Asn	Gly	Thr	Leu	Arg	Gln	His	Thr	Gln	Val	Leu		
625					630					635					640		
Phe	Ile	Ser	Lys	Ile	Thr	Ser	Asn	Asn	Ser	Gly	Ala	Tyr	Ala	Cys	Phe		
				645					650					655			
Val	Ser	Asn	Leu	Ala	Thr	Gly	Arg	Asn	Asn	Ser	Ile	Val	Lys	Asn	Ile		
			660					665					670				

Ser Val Ser Ser Gly Asp Ser Ser Arg Ser Thr Pro Ile Pro Phe Ser
 675 680 685
 Tyr Ser Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp
 690 695 700
 Val Ile Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp
 705 710 715 720
 Ile Ile Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro
 725 730 735
 Asp Ala Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val
 740 745 750
 Asn Asn Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu
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 Tyr Asn Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val
 770 775 780
 Pro Lys Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr
 785 790 795 800
 Ser Ile Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly
 805 810 815
 Trp Ser Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp
 820 825 830
 Ser Ala Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys
 835 840 845
 Phe Asn Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn
 850 855 860
 Asp Arg Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly
 865 870 875 880
 Ser Ala Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile
 885 890 895
 Thr Leu Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile
 900 905 910
 Asp Lys Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu
 915 920 925
 Lys Leu Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp
 930 935 940
 Gly Asn Pro Leu Arg Tyr Asp Thr
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<210> 52

<211> 2359

<212> DNA

<213> Artificial Sequence

<220>

<223> rhCEA-CTBopt fusion

<400> 52

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 cgcccccttca acgtggccga gggcaaggag gtgctgctgc tggcccacaa cgtgagccag 180
 aacctgttcg gctacatctg gtacaagggc gagcgcgtgg acgccagccg ccgcatcggc 240
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 accatccagg tgatcaagga ggacctggtg aacgaggagg ccaccggcca gttccgcgtg 420
 taccgccgagc tgcccaagcc ctacatcagc agcaacaaca gcaaccccgt ggaggacaag 480

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accgtgtttca acatcccccg caacgacacc accagctaca agtgcgagac ccagaacccc 660
gtgagcgtgc gccgcagcga ccccgtagacc ctgaacgtgc tgtacggccc cgacgcccc 720
accatcagcc ccctgaacac cccctaccgc gccggcgaga acctgaacct gacctgccac 780
gccgccagca accccaccgc ccagtacttc tggttcgtga acggcacctt ccagcagagc 840
acccaggagc tgttcatccc caacatcacc gtgaacaaca gccggcagcta catgtgccag 900
gcccacaaca gcgccaccgg cctgaaccgc accaccgtga ccgccatcac cgtgtacgcc 960
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<210> 53
 <211> 784
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> rhCEA-CTBopt fusion

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<400> 53
Met Gly Ser Pro Ser Ala Pro Leu His Arg Trp Cys Ile Pro Trp Gln
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Thr Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
          20          25          30
Thr Ala Gln Leu Thr Ile Glu Ser Arg Pro Phe Asn Val Ala Glu Gly
          35          40          45
Lys Glu Val Leu Leu Leu Ala His Asn Val Ser Gln Asn Leu Phe Gly
          50          55          60
Tyr Ile Trp Tyr Lys Gly Glu Arg Val Asp Ala Ser Arg Arg Ile Gly
          65          70          75          80
Ser Cys Val Ile Arg Thr Gln Gln Ile Thr Pro Gly Pro Ala His Ser
          85          90          95

```

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Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Ser Val Ser
 530          535          540
Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Ile Leu Thr Leu Leu Ser
545          550          555          560
Val Thr Arg Asn Asp Thr Gly Pro Tyr Glu Cys Gly Ile Gln Asn Ser
          565          570          575
Glu Ser Ala Lys Arg Ser Asp Pro Val Thr Leu Asn Val Thr Tyr Gly
          580          585          590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Leu Ser Tyr Arg Ser Gly
          595          600          605
Ala Asn Leu Asn Leu Ser Cys His Ser Asp Ser Asn Pro Ser Pro Gln
 610          615          620
Tyr Ser Trp Leu Ile Asn Gly Thr Leu Arg Gln His Thr Gln Val Leu
625          630          635          640
Phe Ile Ser Lys Ile Thr Ser Asn Asn Ser Gly Ala Tyr Ala Cys Phe
          645          650          655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Asn Ile
          660          665          670
Ser Val Ser Ser Gly Asp Ser Ser Arg Thr Pro Gln Asn Ile Thr Asp
          675          680          685
Leu Cys Ala Glu Tyr His Asn Thr Gln Ile Tyr Thr Leu Asn Asp Lys
 690          695          700
Ile Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile
705          710          715          720
Ile Thr Phe Lys Asn Gly Ala Ile Phe Gln Val Glu Val Pro Gly Ser
          725          730          735
Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr
          740          745          750
Leu Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val
          755          760          765
Trp Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 770          775          780

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<210> 54

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> tetanus toxoid peptide

<400> 54

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Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala
 1          5          10          15
Ser His Leu Glu
          20

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